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Links

Calculating percent identity between protein or DNA sequences with a word processor.

Ladror US.

Department of Biological Chemistry and Structure, University of Health Sciences, Chicago Medical School, IL 60064.

Two macros, to calculate percentage identity between protein or DNA sequences using the Microsoft Word word processor, are described. The user prepares an alignment file of multiple sequences which is used by the macros to calculate number of matches, number of mismatches, total number of compared positions, and the percent identity. The macros are especially useful when alignment of multiple sequences is possible only by eye.

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CEDIT: a C interface and macro facility for protein sequence alignment editing in colour with Microsoft Word. [Biochem Biophys Res Commun. 1993]

Using CLUSTAL for multiple sequence alignments. [Methods Enzymol. 1996]

ALIGNMENT SERVICE: creation and processing of alignments of sequences of oligonucleotides. [J Biol Chem. 1995]

An Eulerian path approach to global multiple alignment for DNA sequences. [J Comput Biol. 2003]

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